



/clone\_lib="Maize Mapping Project/DuPont Cornsensus Library"  
/note="this sequence is part of a project of EST

BASE COUNT  
ORIGIN

615 a	430 c	599 g	538 t	83 others
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assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of Bt23s in conjunction with the Maize Mapping Project".

Query Match 28.4%; Score 472; DB 11; Length 2265;  
 Best Local Similarity 56.4%; Pred. No. 1. 3e-120;  
 Matches 913; Conservative 0; Mismatches 697; Indels 9; Gaps 3

Qy	Db
348 NNNNNNNNNCAGATGCGTCRAAGTGACATGGGACCTAAGGGGGCATGTTGTTATG	407
133 AAAAAGCTTGTGTCCTTAATTACTAATGAGGGGTACCATCTCTAAAGAGATCG	192

QY	DB	408	AGCAAGGCTTTGGCACCCAAAGTCAGCAAAAGGGTGTTGCAAGAGCATTG	467
193		AACTAGAAAGCTTTGAAACCTGGAGGCAAAATTGGTGCTGAGTCGCTCTAA		252

Db	Qy	Sequence	Score
468	RAATTTAGGATAGCTAGTAAAGAATGTTGTCGAAACGTTCTATGGAA	527	
253	CCATGATATGTTGGGATGGGGGACTACTGCAAGTTTGCACACCCATGTC	312	

Qy	Db	587
313	CTTGGAGCTAAAGATGTCACGACGAGTGTCTTCCATGGTTCGAGGCGATG	372

Db	588	CTGAGGGGGTCGAAATCTGTTGCGCTGGAATGATGCGATGATTAGGGGAACT	647
Oy	373	AACAGCACAGAACGCTTGAACCTGTGAAAGCCATGTCACACTGTATCTGGCA	432

708 CAGAKAANAGTGGACGTGGTGGTACATATTCAGAAATGGGAGAAATTGTGCG 767  
 490 ATATCTCAGGAGCTATGGACCGTGGCACGATGGTGTGATTACATCAGAACATTC 549

828	ACACCTTATTATGAGCTTGAATGAGCTTGAAGGTTAGAACTGAGAGGTACACT	887
610	CTCAATACGTGTCAGACAGTAAAGTGTTCAGCTCTGAAACCTTATCT	669

948	TTATTGATGACAGAGGTAGAATGCTGCTGGTTAAGTTTGAATGCCC	1007
730	TTAACACACCGCTCATCTACTATGCGATATCGATGCTGGATGCTGAGAATGCTC	769

1068 CTTGATTATTACAGCTCTGAGGCATCAAGCTCTGCTGCAAGCTCTGTT 1127  
 850 TTGGTATCGTGTAAAGCTATGCTGAGAACATTCTATCTGTGAGGCTGTACAGTA 909  
 |||| ||| - || ||| - | - |||| |||| |||| |||| |||| ||| - || |

Db	1128	TTGGGAAACAGGAGGCAACTACAGGACCTTCGCAATCCTCTTGCGGAGGCTA	1187
Oy	910	TTACAGGAGCTAGCTGAGCTGAAATTAAAGATGCTACATGACAGCCCTTGACAGCTG	969
Db	1188	TACTGAGACTAGGATGACCTTGGAAATTGAGCCTCACAGTCGCGGACAGCTG	1247
Oy	970	CTAAGTTACAGTGTAAAGATGCACTGAGCTGAGCTGAGGTCTAGAG	1029
Db	1248	NNNNGGTACTGCTCTAAGGATGACATGCTATCTGAGCTGAGGAGCTG	1111
Oy	1030	CTPATGCTTACCCCTATGCACTGATTAATGCACTGAGCTGAGCTGAGGAGCTG	1307
Oy	1150	TTAGGCTCCAAACAGGAGACGCTTAAAGAATGAGAACACTTCGACCTG	1089
Db	1308	CTATGAGAGGGAGGAGCTGAGCTGAGTATGAGCTGAGGATGAGATACAC	1367
Oy	1090	ACCGTGAAGAACATACAGAAGCTTGGCAATAUTGCTGGTGTGAGTGTATCAG	1149
Db	1368	ATAAGGAAAGACGCCGGAGCGGTGCGAACAGCTCTCGGGAGGTGTTGAGA	1427
Oy	1428	TTGGAGGACCCAGCGGAGCAGAAGTGTGAGGAGGATAGCTGAGCTG	1487
Db	1210	ATGCCAACCTGCAACGGCTGAGGAGTGTGAGGAGAATGAGCTGAGCTG	1269
Oy	1488	ATGCTACTAAACSTGCTGTGAGGAGGGTAAITGTCACCGGTTGTTGCTCTC	1547
Oy	1270	CGGTTATGAAAGAGGAGAGCCTTCAGCTG---AGGGGAGGATGCTACTGGACGT	1326
Db	1546	ATGCATCGGGGGCTGTATAATTGAGACGGGAACCTGGATGAGGAGATGGTC	1607
Oy	1327	ACATGTTGTTGTTGCTGAGAACGCTTACCTCAATGCTTAAATTGTTGAG	1386
Db	1608	AAATATCTCAGATGCTTGTGAGAACCTTCACACATGTTGCTCAGTGGTG	1667
Oy	1444	CTGCAACAGGTTGGGTTGATGTTAACAGGAGATGTTGAGCTGTCAGTGA	1503
Db	1728	CTGCTAAAGGTGAAATGTTGAGCATGTTGAGACGGGATCATGGACCGCTAAGGTA	1787
Oy	1504	CACCATCAGCTTCAATGAGCTGCTGTTACCTTACTCTTATTGACACAGAGC	1563
Db	1788	TCAGACTGCTTGTGGATGCTGTTGTTGTCCTGATGACACACAGGGATCCA	1847
Oy	1564	TTGTTGCTTAATACCTGACCACTGACGCTGACGCCGACATGCCACAGSTGAT	1622
Db	1848	TAATGTTGAGATTCACAGGAAGGAGGCCGCTCCGACAGTGGTGGCCATGGT	1906
RESULT 2			
AY104969			
LOCUS	AY104969		
DEFINITION	zea mays	2250 bp	mRNA
ACCESSION	AY104962	mRNA sequence.	1 linear
VERSION	AY104969		.HTC 25-MAY-2001
KEYWORDS	HTC.		
SOURCE	zea mays		
ORGANISM	zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC		
REFERENCE	clade; Panicoideae; Andropogoneae; Zea.		
1	(bases 1 to 2250)		
AUTHORS	Haines,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,		
	Arthur,L.W., Hanafey,M., Morgante,M. and Timney,S.V.		
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of		
OVERVIEW	Over 1000 Probes		
REFERENCE	unpublished (2002)		
2	(bases 1 to 2250)		
AUTHORS	Coe,R.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project. University of		



AUTHORS	Coe, E.C.
TITLE	Direct Submission
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES	Location/Qualifiers
source	1..2338 /organism="Zea mays" /db_xref="MaizeDB:633377" /clone="P0063180" /clone_id="Maize Mapping Project/DuPont Cornsensus Library"/> Note: this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration of public overgo addressing of BACs in conjunction with the Maize Mapping Project.
BASE COUNT	668 a 483 c 643 g 544 t
ORIGIN	Query Match
Best Local Similarity	25.9%
Matches	875; Conservative
Pred. No.	5..26..109;
Mismatches	669;
Indels	13;
Gaps	3;
QY	66 GGAGTGTAGATCTAGAGATACCGCTCAAGTAACGCTGGCTAAGGGCGATGTT 125
Db	452 GGAGTGTAGATCTAGAGATACCGCTCAAGTAACGCTGGCTAAGGGCGATGTT 511
QY	126 GTCCTGAAAGAACCTTGTGTCCTTAATTACTATGACGGGTACCTGCTAA 185
Db	512 GTTGTGAGAGCAGTCAGTCAGGCTCCCAAGATGTACAGTGCGCTTACAGTCAGA 571
QY	186 GGAGATGAAATAGAAAGTCTTGTAAACATGGGCGAAATGGTGTCTGAACTGGCT 245
Db	572 GGGGTGACTGGAGGAGCTGTGAGAAACCTTGTGAGCTTACGGCAACTGCTCA 631
QY	246 TCTAAACCAATGATATTGTGGTGTGGAGACACTTGCAACAGTTGACACACC 305
Db	632 GCTAACGACCAAGCATCTGCTGAGGAGCACACCTCTGGCTCTGCTCAGGG 691
QY	306 ATCTGTCACTGAGGAGTAACAAATGACGAGCGTGTACATGGTACGGCA 365
Db	692 CTGATGTCGAGGTTTAAAGTTGTGCGAGCTGCTGCTATCTGTGCTAGATGGT 751
QY	366 GCGATGAAACAGCACACGCAACAGAGTGTGAGGCTCTGAAGGCCATGCTCAACCTGA 425
Db	752 GGTATGCGAACACGCAAGGAGCATGAGTGTGAGAATACGGAGTTGCTAAGGAGTT 811
QY	426 TCTGCAGAAGACTATCTCGAGTGTGCGTCAGTCACCGCTCTGAAGAATGCGA 485
Db	812 GAGAGATAGTCGAGCTTCAGATGTTGTGCTGTTAGCTGCAACAACTATGAAATTGT 871
QY	486 GAGTATACTCGAGACCTGTGAGGCTGTGAGGAAACGATGTGTGATGATGTTACCATGAGGA 545
Db	872 AACATGATGAGCAGAGGCCATGCGAACGGTGTGGTACCTCGACAGAG 931
QY	546 TCTCGAGTATGGAGACAGCTTGTGAGTGTGAGGCTGTGGTAC 605
Db	932 GGGAGACTTCGACACTTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 991
QY	606 CTGTCATCATGTCAGTCACAGACATGAAATGTCAGACCTGAAACCAATT 665
Db	992 ATCTCTCGTGTACTTGTGAGCAGACTGTGAGGAGTGTGAGGAGTGTGAGA 1051
QY	666 ATCTTAACTCAGGATAAAATGTCAGAACATCAGACATTGTGCCAC-TACTGTGGA 724
Db	1052 CTGTTGAGGAGCAGAACAGTCACCGAGGAGCTTACCATTTGGAA 1111
QY	725 AGCTTTAAACCAACGGCCATTACTCATTAATGAGATGAGGTGGAGACT 784
Db	1112 AGCCATCAGAGGAGTCACCCAATCTGTAATGTGAGGAAATTGAGGCTCT 1171
RESULT	4
BH70613/C	
LOCUS	BH70613
DEFINITION	1327 bp DNA sequence
ACCESSION	LM37372
VERSION	MG1363
KEYWORDS	Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, DNA sequence.
GSS	BH70613.1
ORGANISM	Lactococcus lactis subsp. cremoris.
Bacteria: Firmicutes; Lactobacillales; Streptococaceae; Lactococcus.	
REFERENCE	(bases 1 to 1377)
AUTHORS	Boletin,A., Enrich,S.D. and Sorokin,A.
TITLE	Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL	Sci. Aliments, (2002) In Press
QY	785 TCCAAACCTGCTTCAGACAGATGTTGACTTCATGTTGTTGAGTCAGGGCC 844
Db	1172 TGCTACCTGTGTCGTCACAGCTCGAGGATCACTGAAAGTCGCTGCACTAAAGCC 1231
QY	845 AGGATTTGTGTCGCGTAAGCTATGCTGAGACATGCTACTGTGAGCTGAGTC 904
Db	1232 TGGTTGAGGAGCCAAAGACTGACTTGTGAGATGATGATGAGGAGTCAC 1291
QY	905 AGTGTATCAGAGATCTGGACTGATTAAGATGCTPAATGAGCCCTGGACA 964
Db	1192 TGTAAATCAGAGTGAATGTTGGCTGCACTGACAGCGCTACATTGCTCTGGAC 1351
QY	965 GGCTCTAGATTACAGTGTAAAGATACAGACAGTAAATGTTAAGGTGGAGTC 1024
Db	1152 AGCTCAAGGTGTCCTACAGAAGAGTGCACAACTATGTTGTTGAGGAC 1411
QY	1025 AGAAGCTATGCTAACCGTATCAGTAAATGCCAATTAAGACACACACTCTGA 1084
Db	1412 GGAGAACTACTAGAGGTTGCGAGAGTAAATCTCATGAGGCAGGACAGA 1471
QY	1085 CTTGACCGTGRAAACATPACAGAAGCTTGGGAAATTAGCTGTTGTTGAGCTAT 1144
Db	1472 ATATGAAAGGAAAGCTCAATGAGGAGATAGCAAGCTGCTGGTGTGTTGCT 1531
QY	1145 CAAAGTAGACTCTCAAGAGAGACGCTTAATAAGAAATGAACTCGCATTGGATGC 1204
Db	1532 TCACTGGAGCACAAAGACAGTAACTAAAGTAAAGGAGCTCTGCTGAGTC 1591
QY	1205 TCTAAATGCTCACCGTGCAGCGCTGAGAACAGTATGTTGCTGTTGAGACAGACT 1264
Db	1592 CCTAAATGCAACAGGTTGCTGAGGAGTATGTTGTTGGAGGAGTCACCT 1651
QY	1265 TATRACGTTGTTGAAAGTGTGAGCAGCTCTGACTTAAAGGAGAGTGTGAGGAGTC 1315
Db	1652 TTTCGGGCTTCAGCTAAAGTGTGAGGCCATCAGGATACCTGGAGACATGAGCAGAA 1711
QY	1316 TACRGGGTTACATTGCTCGCTGCTAGAGGCTGTCAGTCATAATGCTTAA 1375
Db	1712 GGTGGAGCTGAAATGAGTAAAGGAGGCTCTGACTCCACTTAATGTTGCTCAA 1771
QY	1376 TCTGGGTTAGAAGGCTGCTGAGTATGACAGTGTAAACAGGCCCTGAGAA---C 1412
Db	1772 TGCCTGGCTCACTGAGCCGGCTGCTACTGAGGAGGCTCTTAAAGATACCTCAGTA 1831
QY	1433 AGGATTAATGCTGCAAGGTTGTTGTTGTTGAGGAGGCTCTGACTCCACTTAATGTTGCTCAA 1492
Db	1832 TGGTACAGCTGCTACTGACAGTGTGAGGAGCTGAGTGTGCTGCGTGTGTC 1891
QY	1493 TGTCAAGTACAGCATGAGGCTCTAAATGACAGCTCTGAGCTGAGTC 1552
Db	1892 TACTAAGTGTGAGATGCTGTTGGAGCATGCCGTTGGGCGCAAGCTCTGTC 1951
QY	153 AAGAGAGCTGTTGCTATAACCCGACGCTAGGCCAGCCAGCAGTC 1609
Db	1952 ATCTGAGTTGTTGCTGATTAATGAGGAGCCAGCTGCTGCGCCCTTGCTAAC 2008

COMMENT	Contact: Sorokin A Genetique Microbienne INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France Tel: 33 1 34 65 25 16 Fax: 33 1 34 65 25 21 Email: sorokin@jouy.inra.fr best homologue in strain IL403 is groEL (93%) Class: shotgun High quality sequence start: 30 High quality sequence stop: 1299. Location/Qualifiers	FEATURES source
BASE COUNT	392 a	1. 1327 /clone_id="MG1363" /organism="Lactococcus lactis subsp. cremoris" /strain="MG1363" /db_xref="taxon:1359" chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
ORIGIN	292 c 239 g 403 t	1 others
Query Match	24.9%; Score 414.2; DB 17; Length 1327; Best Local Similarity 72.0%; Pred. No. 1.e-104; Mismatches 214; Indels 1; Gaps 1;	
Matches	553; Conservative 0; Mismatches 214; Indels 1; Gaps 1;	
Qy	830 TGTCTGCAAGGCCGAGGATGGTGTGATCTTGTGAAAGCTATGCTTGAGACATCCAT 889	
Db	1322 TGTCTGAAAGACCGGGATGGTGTG-CCACCGTAAGCTCATGAGTATAGCTAT 1264	
Qy	880 CTGAGACAGTGATGAGTGTACAGATTAACAGAGGTCTAGGACTGATTAAGATGCTACAT 949	
Db	1283 CTGAGACAGTGATGAGTGTACAGATTAACAGAGGTCTAGGACTGATGCTTAAGATGCTACAT 1204	
Qy	930 GACAGCCCTGTGAGCAGCTGCTAGATAGTGTAGATAGTGTAGATAGCAGTATAGTGTGA 1009	
Db	1203 AGAACCTTGTAGCAGCCTGACAGTGTAGATAGTGTAGATAGCAGTATAGTGTAGATAGTGTGA 1144	
Qy	1010 AGGTCAGGAGTCAGAAGCTATGCTAACAGGATGACTGATTAATGCTATTAGA 1069	
Db	1143 AGGTCAGGAGTCAGAAGCTATGCTAACAGGATGACTGATTAATGCTATTAGA 1084	
Qy	1070 AACACAACTCTGACTTGACCGTAAACATACAAAGAAGCTTGTGGAAATTAGCTG 1129	
Db	1083 AARAAATACCTGTGTTGGCGTGTAAAGATGCAAGGCCTAGCGAAATTAGCTG 1024	
Qy	1130 TGGTGTACCTGTATCAAGTAGGACTCCACAGAGCAGCCTTAAGAAAGAACT 1189	
Db	1023 CGGAGTTGGTAGTAAAGTAGGAGGCCAACAGAACAGTAAAGCAATGAACT 964	
Qy	1190 TCGCATTCAGGTGTCTAAAGTCCTACGGTCTGGCGGTGAGAAGAAGTGTGCGG 1249	
Db	963 TTGATGAGCAGCCTATACATACACAGCTGCTGTTGAGAAGGATGTTGCG 904	
Qy	1250 TGGTGAACGACTATACATGCTTGTGAAAGTAGTGTAGCTGTGTTGAGA 1309	
Db	903 TGGTGTACAGCTGTGTTGAGCCATCGACGTTGAGAAGGAGG 844	
Qy	1310 TGATCCTACTGCGTACATGCTGCTGCTGCTAGAAGAGGCTGTACGTCAATGCG 1369	
Db	843 CATTCAAAGAGGATTAATCATCTTGGCGTGCCTGTAGAACGCACTTCGTCAATGCG 784	
Qy	1370 TTAAATCTGCTGAGGCTGCTGTTGAGTGTAACTTGCAACTTGTGAAACGCCGCG 1429	
Db	783 GGCCATGAGGATGAGGAGTCACTTGATGAAAGTGG 724	
Qy	1430 AACAGGATTAATGTGCAACAGGAGGGTGTAGATGATTAACAGAACTATGCA 1489	
Db	723 TACAGGATTAAATGCGCACAGGCAATGGTAATATGAGAGGAAATGCG 664	
Qy	1490 CCCTGCAAGAACGAGTCAGCGCTCAAATGCGCTCTGTCTGAGGATGTT 1549	
BASE COUNT	546 a	1. 2143 /organism="Zea mays" /db_xref="MaizeDB:630266" /db_xref="taxon:577" /clone_id="PO140434" /clone_id="Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes Unpublished (2002) 2 (bases 1 to 2143) Coe,E.C.
ORIGIN	494 c 598 g 505 t	
Query Match	23.1%; Score 383.6; DB 11; Length 2143; Best Local Similarity 54.0%; Pred. No. 7.e-96; Mismatches 734; Indels 16; Gaps 4;	
Matches	880; Conservative 0; Mismatches 734; Indels 16; Gaps 4;	
Qy	18 GCAAGAAATCAATTTCAGCAGATGGCGGTGTGCGATGTTGGCGGAGTTGATAC 77	
Db	274 CGCAGGAGTCGCGCTTGTACGACGCGCAGCGCGCTCAGCGCGCTCGCG 333	
Qy	78 TTGAGATACCGGCAAGTACCTGCTGTGCTAAAGGCGCAATGTTGCTGAAAN 137	
Db	334 CTGGCCCGGGTGGCTACCCCGACGAGGATGTTCTGAGGATGTTCTGAG 393	
Qy	138 GCTTTGTTCTCTTATTAATCATGACCGGGTAACTATGCTAAGAGATGATA 197	
Db	394 --TTGAGACCCCAAGTGTGTCATGATGAGTGGAGTACATGCCGCGCTATGCGT 450	
Qy	198 GAGATCATTTGAAACATGGGCAAAATGGTGTAGAGTGCTCTAACACAM 257	
Db	451 GCGATCCATGAGAATGCGTGTGCTTCAGTGTGCGCAGACGAAAT 510	
Qy	258 GATTCCTGTGAGGGACAC-TACGCAAGCTTGTACACAGCCTGTCAG 316	
Db	511 GACCTGCGCTGTGTTGAGACCAACAGCCTGCTGCTGAGGATCATCAAT 570	
Qy	317 AGGACTAAAATGTCGACAGGTCGAAACATTGCTTCCCTGAGGCAATC 376	

Db	571 GGCAGATGTTGACCAATTCTCAGGSSCAAATCCAGTCGCGTTAACAGGGCAATGATAA 630	Qy	1445 TGCACAGGTGACTGGGTATGATTAACGGATCATGTACCGCTGTCAGTAC 1504
Qy	377 AGCACACGACACAGCTGTTGAGCCTTGAAAGCCATGTCACCGCTATCTGGCAGGA 436	Db	1711 CATGGCAGACAGCAGGAACTTGAGGAAATCAGGCCGTCAGGTTGG 690
Db	631 GACTGTGCAAGATGTTGGTGAGGAACTTGAGGAAATCAGGCCGTCAGGTTGG 690	Qy	437 AGCCTATGCTCTAGGCTGGCTGAGATACATCAGCAGCTGTCAGTCTGAAAGTGGAGAT - - - 493
Qy	691 CGATTTAGCTAGGCTGGCTGAGATACATCAGCAGCTGTCAGTCTGAAAGTGGAGAT - - - 493	Db	1711 TAGTGCGCCCTGAGAACTGCTGCTCGTGCGTGAATGTTGAGATGGCTGATGATC 1830
Qy	494 CTGAGAGCTCTGGAGCTGGCTGGGAAACATGGTGTGAAATACCATGAGAATCTCAGG 553	Db	1565 TGTCTCTATAACCTGAGACACTGCGAGGCCAGCAATGCGCAGGTTGGATGATC 1624
Db	751 CGCGGAAGCTTGTGACGAAAGGTGGCCCTGATGGTGTGCTCTCATGGTACGTC 810	Qy	1831 CCTGGGAGAACCCAAAGAGCTCCAGGAGCAGCTGCTCAGGGTC 1890
Qy	554 TATGAAACAGACAGTGTGAGTGTGAGGTTGAGGAGGGGTGAGGAGCTGTGTC 613	Qy	1625 AGGAATGTC 1634
Db	811 GTTGTGAGACACAGTGTGAGTGTGAGGTTGAGGAGGGGTGAGGAGCTGTGTC 870	Db	1891 TTTCACCATG 1900
Qy	614 ATACATGTCACAGACAGTGTGAGTGTGAGGTTGAGGAGGGGTGAGGAGCTGTGTC 673	RESULT 6	AY106465
Db	871 TCACTTGTCACATGAAATGTCAGGATGTCAGGATTAATGTCAGGATATCTCAAT 930	DEFINITION	AY106465
Qy	674 CACCGATTAACAAACGTCACACATCAAGACATTGCACTACTTGAGGAATCTAA 733	DEFINITION	Zea mays mRNA sequence.
Db	931 CACTGATGCAAGAGATATCATGGTAAAGAAATTATCTCTCTGAGCACACACA 990	ACCESSION	AY106465
Qy	734 AACCAACCGTCATACATACATATGAGATGATGGATGGAGCACTTCACACCT 793	VERSION	AY106465.1
Db	991 GTTAAAGACACACTCTTATTTGCAAGGATTAATGTCAGGATATCTCAACACCT 1050	KEYWORDS	HTC
Qy	794 TGTCTTGACAGAGTCTGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGT 853	SOURCE	Zea mays
Db	1051 AGTCATAACAGACGTTAGGAGATTTAAATGTCGCAACAAAGCCTGTTGG 1110	ORGANISM	Zea mays
Qy	854 TATCCGCTGTRACGCTGTGAGTGTGAGACATCTCTGAGAGGGGACATGTAC 913	REFERENCE	Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; clade; Panicoidae; Andropogoneae; Zea
Db	1111 TGGAGGGCTAACTCTCTCTGAGAGATTCAGGCTTGTACGGGCTGAAATATC 1170	REFERENCES	1 (bases 1 to 1176)
Qy	914 AGGAGCTGAGCTGTGAGTGTGAGGAGTACACAGCTGGAGCTGCTGAA 973	AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanley, M., Mongan, M. and Tingey, S.V.
Db	1171 CAAGATGCTTGTGAGTGTGAGGAGTACACAGCTGGAGCTGCTGAA 1230	TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Qy	974 GATTACAGTGTGAGTGTGAGGAGTCAGGAGTCAGAGCTT 1033	JOURNAL	Unpublished (2002)
Db	1231 AGTACATCTCAGTCTCTGAGCCATTAGCAGATGTCAGAACAGCTAT 1290	DOI	2 (bases 1 to 1376)
Qy	1034 TGCCTAACCGTATCTACGTAATAATCGCATTACAAACACACTTCGACCTG 1093	NOTE	See E.C.
Db	1291 CAGGCCAGATGCGGCTGAGAGAGACCTTCTCAGAGGACTTCAGCTAC 1350	DIRECT SUBMISSION	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Qy	1094 TGAACAACTACAGACAGCTGTTGGAAATGACTGTGTTGAGCTGTTAATG 1153	FEATURES	Location/Qualifiers
Db	1351 TGAAGACTTGCGAGAGAAATGCGCTTCTGGAGTGTGTTGGT 1410	Source	1. 1..1376
Qy	1154 AGCTCCACAGACAGCTTAAAGAAATGAGCTGGCATGAGGAGCTGCTAATGC 1213	Organism	"Zea mays"
Db	1411 AGCATGCGACCGAGCAGCTAGGGAGCCAGSTCGCGATAGGAGGCG 1470	Db_xref	"/db_xref="MaizeDB:637486"
Qy	1214 TACACCTGCGACGCTTGAGAGGATGCTGTCGTCGACAGCACTTAATGGT 1273	Clone_id	"Maize Mapping Project/DuPont Consensus Library"
Db	1471 GACTTGTGACGAGTATAGGAGGATGAGGAGCTGCTGAGGAGCTGCTAATGC 1530	Assembly	/note-- this sequence is part of a project of EST contigs to seed BAC contigs; this resource was assembled by BACs as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize
Qy	1274 TATGAAAGATGACGACTCTGTGAGCTTGAGGCTCATGTCATGTGACG - - - 1324	Project"	Mapping Project"
Db	1531 ATGGCAGCTGCTGAGGCTATCAAGGAGACGCTGTTGAGATCTGAGGCCCTAGGG 1590	Base count	397 a
Qy	1325 TAACTGTTGCTCTGCTCTGAGAGACCTGCTGAGTAAATGCTTAAATGCTGGA 1384	Query Match	18 2%
Db	1591 TGTATATCATGAGCTTGGGGACTCTGAGCTGAGGAGCTGAGTAACTGGT 1650	Best Local Similarity	Score 302.8; DB 11; Length 1376;
Qy	1385 CGAGGGCTGGTTGTTGAGCAAGTGTAAACACGCCCTGAGGACAGGATTATGC 1444	Matches	55.7%; Pred. No. 2, Se-73;
Db	1651 GGAGGTGAGGTTGATTAATCGGGAAAGCGACTGGTGGCTACACCC 1710	Best	0; Mismatches 487; Indels 6; Gaps 2;
Qy	478 NAGTGGAGATATCTCAGGATCTGAGCTGAGGCTGTTGGCCACGATGTTGATTC 537	Db	23 AAATGGAGCTTAAATCAAGGACATGAAATCTGAGGATGGCTACTACTA 82
Qy	538 TCGAGAGATCTCGAGTATGAGAACAGCACTGAGCTGAGTGTGAGGATGCAATGACC 597	Db	83 TTGTGATGGCAACATGGAGCATGAGTGGCTGAGCTACAGGGATGAGCTGTC 142
Qy	598 GTGGTACTCTGCACTGAGCTGAGGAGCTGAGGAGCTGAGCTGAGCTGAA 657	Db	143 GAGGATCATCTCTCTTGTGACTGATGAAAGACTCAGAAATGTTGAGATGGAGA 202



QY	1108	ACGTTTGGCAAATTAGCTGCGGCTGAGCTTCAAGTAGGAGCTCCAAAGAGA	1167	JOURNAL	Submitted (09-SEP-2000). Genoscope - Centre National de Séquenage, 2 rue Gaston Crémieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail: seqr@genoscope.cnrs.fr) ; Web : <a href="http://www.genoscope.cnrs.fr">www.genoscope.cnrs.fr</a>
Db	554	AGAGAACTGAACTGCTGGGGGTTGGTGTGTTGTTGATGCTGAGCTGAGA	613	COMMENT	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>vararium</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces lactis</i> , <i>Kluyveromyces hanseensis</i> var. <i>hanseni</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
QY	1168	CGCTTAAAGAAGAAGTCTGTTAGCTTAACTGCTGAGCTGAGCTGAGG	1227	FEATURES	Location/Qualifiers
Db	614	CAGCTTGGAGCCGAGCTTAAAGAAGTCTGTTAGCTTAACTGCTGAGG	673	source	1. -887 /organism="Kluyveromyces lactis" /strain="CLIB 210" /variety="lactis" /db_xref="taxon:28985" /clone_id="B00A0B027507" <4...>887 <note>"similar to <i>Saccharomyces cerevisiae</i> ORF YLR259c [HSP60 ; heat shock protein - chaperone, mitochondrial ]" <note>"similar to <i>Saccharomyces cerevisiae</i> ORF YLR259c [HSP60 ; heat shock protein - chaperone, mitochondrial ]", evidence-not experimental
QY	1228	TGAAAGAGGTACCTGTTGCGGCTGAGCTGAGCTGAGG	1278	BASE COUNT	256 a 163 c 216 g 252 t
Db	674	TGAGAGGGCTGTCTCAGGCTGAGCTGAGCTGAGG	733	ORIGIN	Query Match 15.8%; Score 263.2; DB 17; Length 887: Best Local Similarity 58.7%; Pred. No. 2.4e-62; Mismatches 343; Indels 4; Gaps 2; Matches 493; Conservative 0; MisMatches 343; Indels 4; Gaps 2;
QY	1279	AAAGTAGGACGCTCTGAGCTGAGGCTGATGCTACTGGAGG	1338	QY	21 RAAAATCAATTAGAGATGGCTGAGCTGAGGCTGAGTCTGAGAAGCT 80
Db	734	CTAACATCAAAGAAGCAATGAGGACCCCTGATGAGG	793	Db	25 AAAGAATAAAGTTGGTTGAAGGTAGGCCTGCTGTTAAGGGTGTGAAACCTA 84
QY	1339	GGCTCTAGAGGCGCTGACGCCATTAACTGCTTAACTGCTGAG	1398	QY	81 GCAGATACGCTCAAGTACCGCTGTCCTAAGGGCGAAGTGTCTGAGAAGCT 140
Db	794	ACGATTTGGTAGCCTGCTCATGTTACACAGCAGGCTGAGG	853	Db	85 GCGGAAGCTGTTGCGCATTTGGTCACAAAGTTGAAAGTGTGACACCA 144
QY	1399	TTATGACAGTGTAAACACCCCTGAGGCTGTTGATGCTACTGGCTC	1457	QY	141 TTGGTCTCTTAACTCTAACAGGGAAACATGCTAACAGATGAGTAAAGCT 200
Db	854	TGTCGAGAGATCAAGGCGAGGATTTGGGGCTACATGAACTGAG	913	Db	145 TTGGCCCTCAAAAGATCACCRAGATGGTTACGGCTACTTGGAA 204
QY	1458	TGGTTGATGATTTAAACAGGATCATGACCCCTCCTAAAGAAGCT 1517	QY	201 GATCATTTGAAACATGGGACAATTTGGCTGAGTGTGCTGAGTCTAAACCAAGAT 260	
Db	914	TCGAGAACCTGTTGAGGCTGCTGGTGTGATGACCCCTCAGGTC	973	Db	205 GATAGTTGCAAAACATGGGCTGAGCTTACAGAGTGTCTTCAGAACAGAA 264
QY	1518	CAATGCGCTCTGAGCTTAACTGCTTAACTGCTTAACTGCTTAA	1577	QY	261 ATGGCTGTTGAGGACTCTGCAACATTGACACAGCCATTGTCATGAGGA 320
Db	974	CGAGATGCGCTACTGCTGAGGCTCTAACACAGCAGGCTGAGG	1033	Db	265 GCTGCCGTTGAGCTTACCTCTCCACTGCTTGTAGTAAAGCCATTCTACTGATCC 324
QY	1578	CTGACCCGCTTGGCCAGGCCAGCAATGCCAACAGG	1615	QY	321 CTAAATATGAGCAGGAGGCTTACATCAATTGATCAGTGTGCTGAGACAGCA 380
Db	1034	CCAAAGCCGCTCAAGTGGCAAGGCCACCGAGGG	1071	Db	325 GTTAAGATGTTGCAAGTGTGAGCTTACAGGAGGAGTCAAGCTGCT 384
RESULT 8				QY	381 ACAGCACCGCTGAGGCTTGAAGCCATTGCTCAACCTGTATGGCAAGGAGCT 440
CNS074DM				Db	385 GTGAGAAATTAATCTTCTGAGCAAGAGAAGAACCTTGTGAA 444
DEFINITION	CNS074DM	887 bp DNA linear	CLIB 210	QY	441 ATGGCTGAGCTGCTGAGTACATGCTGAAAGTGGAGGATATCTCA 497
ACCESSION	BA00B027B07	clone BA00B027B07: of 1 library BA00 from strain		Db	445 ATGGCTGAGCTGCTGAGTACATGCTGAAAGTGGAGGATATCTCA 504
VERSION	AL028672.1	library BA00		QY	498 GAAGCTGATGAGCTGCGGAGATGTTGATGCTGAGCTTGTGTTGCT 557
KEYWORDS	GSS			Db	505 TCAGCTGAGAAAGTGTGAGGAGGTTCTCATCTATGAGAGGCTAACCTG 564
SOURCE	Kluyveromyces lactis			QY	558 GAAACGACATGAGTGTGAGGCTGAGTGTGAGGCTAACCTGTTCTCAATAC 617
ORGANISM	Kluyveromyces lactis			Db	565 GAAGATGAGCTGAGGAGCTGAGGTTCTCATCTAACCTGTTCTCAATAC 624
REFERENCE	Bukalo, J., Fungi; Saccharomycotina; Saccharomycetes; Saccharomyces; Kluyveromyces; Kluyveromyces lactis, genomic survey sequence.			QY	618 ATGGTCACAGACATGAAAGATGGTGCAGACCTGATGAAACCCATTATCTAATCAGC 677
AUTHORS	(1 bases 1 to 887)				
TITLE	Souciet, J. L., Aigle, M., Artiguena, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brotter, P., Casaregola, S., De Montigny, J., Dujon, B., burres, P., Lepingle, A., Liorante, B., Maupertuy, A., Neveuville, C., Olier-Kalogeropoulos, O., Peltier, S., Saurin, W., Tekka, F., Toffano-Noguès, C., Wesołowski-Louvel, M., Wincker, P., and Weissenbach, J.				
JOURNAL	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies				
MEDLINE	FEMS Lett. 267 (1), 3-12 (2000)				
PUBMED	1084711				
REFERENCE	2 (bases 1 to 887)				
AUTHORS	Boilotin-Fukuhara, M., Toffano-Noguès, C., Artiguena, F., Blandin, G., Casaregola, S., De Montigny, J., Dujon, B., Lepingle, A., Liorante, B., Maupertuy, A., Neveuville, C., Olier-Kalogeropoulos, O., Peltier, S., Saurin, W., Toffano-Noguès, C., Wesołowski-Louvel, M., Wincker, P., and Weissenbach, J.				
TITLE	Kluyveromyces lactis of the hemiascomycetous yeasts: 11.				
JOURNAL	FEMS Lett. 267 (1), 65-70 (2000)				
MEDLINE	1084721				
PUBMED	11152866				
REFERENCE	3 (bases 1 to 887)				
AUTHORS	Genoscope				
TITLE	Direct Submission				

Db	625	TTATTAACGGACCTAACTGGTAAGTGGATTGARAAACCTTGATCTATGGT	684	Oy	198	GAACATTTGAAACATGGGACAAATTGGCTCGAAGTGCTCTAAACCAAT	257	
Oy	678	GATAAAAGTGTCAACAACTTCAAGCATTTGCACTACTTGAGGAGTGCTTAAGC	737	Db	302	AACTATAATCAGAACATGGTCAACTTGCTCTTGCAATGATGACAT	361	
Db	685	GAAGAGAGATCCTCCCACTCCAGGATATGCTCTCTGGTAATGTCACAAACC	744	Oy	258	GATTTGCTGTGAGGGACGACTACTGCACTAGTTTACGAAACCCATGTGAGA	317	
Oy	738	AACCTCCCTACTTATGAGATGATGGATGAGACTCCACCTTGTC	797	Db	362	GAAGAACCTGGGGGCACTTACACTGCTACTGFACTGAGCCTCTATGCAAGGA	421	
Db	745	AGAGACCTGTGATCATGCCGAGATATGATGGC-ACTTTGGCTGCTGTAT	803	Oy	318	GGCTAAATGTCAGCAGCGATTGCTGAACGCCGAGTTGGTAT	377	
Oy	798	TGAACTAGATCGGGTACTTCATGTTGCTCTCAARGGCCGAGTTGGTAT	857	Db	422	GGCTCCGAGAGATGACAAAGGTCTTACCTAGTGGAAAGGTGATGTTA	481	
Db	804	TGAACTAGTGTGAGGTCAAGTTCAGTTGRCCTTAAGCTCAGGTTGGTAT	863	Oy	378	GCAACACCAACAGCTGTAACGCATGCTCACCTATCTGGCAAGGAA	437	
RESULT 9								
LOCUS	BM799922	1090 bp mRNA linear EST 05-MAR-2002		Qy	438	GCTTTCTGAGGCGCAGTGTGAAAG--TTGGAGTATTC	494	
DEFINITION	ACBNCDRT-6417164 NTH_MGC_67	Homo sapiens cDNA clone IMAGE:5492101		Db	542	GAATTGACAGGTTGCTTACATTGCAAAATTGCAATATTC	601	
REFERENCE	5', mRNA sequence			Qy	495	TCAAGACCTGGGGTGGTGGACATGCTGTTGATACATCGA	554	
AUTHORS	(bases 1 to 1090)			Db	602	TCTGATGCAATGAAAGTGGAGAAGGGTGCATCAGTAAAGTGAAAC	661	
ACCESSION	BM799922			Qy	555	ATGGAAACAGACTGAGTGTGAGGCGTACCTGAAAG--TTGGAGTATTC	614	
VERSION	BM799922.1	GI:19116745		Db	662	CTGATGATGATGAAATTATGGAGCTGAGCATGAGCTGAGGCTATTC	721	
KEYWORDS	EST.			Qy	615	TACATGCTCACAGCAGTGAATAATGGTGGAGAAACCATTAATCTTAATC	674	
SOURCE	human.			Db	722	TACTTTTATGATCAAAGGTCAGAATGTTGATTCAGTCAGTGTGAAAC	781	
ORGANISM	Homo sapiens			Qy	675	ACGGATTTACATGCAACATCAGACATTGCACTACTGAGGAACTCTAA	734	
COMMENT	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Db	782	AGTGAAGAAGAAATTCTAGTATCCAGTCATGTTGACTGCTGAAATGCCATGT	841	
JOURNAL	Unpublished (1999)			Qy	735	ACCAACCGTCATTCATGAGTGTGAGCTGCACTGTTGAGCTGAAACCCCT	794	
CONTACT	Robert Strausberg, Ph.D.			Db	842	CACCGTAAAGCTTGTGCTCATATGCTGAGTGTGAGGAACTCTAA	901	
TISSUE	Procurement: ATCC			Qy	795	GCTTGAACAGATTCATGAGTGTGAGCTCATGTTGTTGCAAGCGCAGATTTG	854	
PREPARATION	Life Technologies, Inc.			Db	902	GCTTGAACAGATTCATGAGTGTGAGCTCATGTTGTTGCAAGCGCAGATTTG	961	
CDDA	National Institutes of Health, Mammalian Gene Collection (MGC)			Qy	855	GATCGCGTAAAGCTATGCTGAAAGATGCTATCTGAGGGGGTCACTGATA	914	
DNA	Sequencing by: Agenourt Bioclience Corporation			Db	962	GACATAGAAAGACAGCCATAAGATATGGCTATGCTACTGGGGCCAGGTG	1021	
SEQUENCING	DNA distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>			Qy	915	GAGGACTCTGAGCT 928		
PLATE	ILAM1213	row: k column: 14		Db	1022	GAAGAAAGGATT 1035		
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/lab_host="DH10B (phage-resistant)"								
/note="Organ: eye; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SphI; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.75 kb. Library constructed by Life Technologies."								
BASE COUNT	332	a 209 c 274 g 275 t		RESULT 10				
ORIGIN				LOCUS	BP27584			
Query Match	15.89;	Score 262.8; DB 14; Length 1090;		DEFINITION	BP27584			
Best Local Similarity	56.28;	Pred. No. 3. 6e-62;		ACCESSION	BP27584	Gossypium arboreum		
Matches	514;	Conservative 0; Mismatches 397; Indels 3; Gaps 1;		VERSION	BP27584	7, 100 dpa fiber library.		
Oy	18	GCAAGAGAATCAATTTCAGCAGATGGCTGGCGCATGCTGGCGACATGAT	77	KEY WORDS	BP27584.1	Gossypium arboreum		
Db	122	GCAGGATGATTAATTTGGCGATGCCAGCCTATGCTCAAGGTGATGACCT	181	EST.	GI:11206654			
Oy	78	TTCAGCATGCTGGCAAGTACGCTGCTTAAGGGCATGTGCTCTGAA	137	SOURCE		Gossypium arboreum.		
Db	182	TAGCGCATCTGGCGCTTACATGGCCGAAGGGAGAACGATGTTGACCT	241	ORGANISM		Bulbosa; Vindobonae; Serpophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		
Oy	138	GCTTGGTCTCCATTACTATGACGGGTACACATGCTAAAGATGAGATGAGTA	197	REFERENCE				
Db	242	AGTTGGGAAGTCCAAAGTACAAAGATGTTGAGCTGCAAGCAATTGACTA	301	AUTHORS				
				TITLE				
				JOURNAL				
				NOTE				
				UNPUBLISHED				



	FEATURES	LOCATION/QUALIFIERS
	SOURCE	1. .977 /organism="Zea mays" /cultivar="C0128" /db_xref="taxon:577" /clone="Zm04_04909"
Db	296 AAAGATAATAACAAAACATGGAGCTAACATTCTCAGATGTTGCCAAATACACAAT 355	/tissue-type="Leaf, crown" /vector="Bluescript SK-/XbaI-EcoRI; Site_1: Eco RI; Site_2: Xba I; Lower temperature 50 C / hour from 22 to 120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 days photoperiod 16 hours. Light intensity was 12000 lux-1 library prepared by in vivo mass excision from amplified
Qy	258 GATAATGCGGTCATGGAGACTACTGCACAGCTTGCACAGCAACGATGTTCTGAGA 317	
Db	356 GAAGAGCCTGGGGATGCACTACACAGCCTACAGTCATGTTCTCGGGATGCAAGA 415	
Qy	318 GGACTAAAGAATGTCGACACAGCTGTAACCAATTGTTCTCGGGATGCAAGA 377	
Db	416 GGCTTCGAGAGATTAGCAGAAAGTGCATGGCTGAAATGAGGAGGAGGTTGTTA 475	
Qy	378 GCACAGCAGACAGCTGTTGAACTGAAAGCCTGCACTGTTGCACTGTTGAGCTA 437	
Db	476 GCTGTTGATGCTGTAATGCTGACTTAAAGCAGTCTAACCTGTGACCGAA 535	
Qy	438 GCTATTGCTCAGTCGCTCAGTACAGTACAGCTGAAAGCCTGCACTGTTGAGCTA 494	
Db	536 GAAATGCGACAGCTGCTGAGTTCTGAAAGCAGACAGAAATGGCAATCCTC 595	
Qy	495 TCAGAGCTATGGGGTGGCCACAGATGTTGTTACCTCGAGAATCTCGAGGT 554	
Db	596 TCTGATGCTGATGAAAGAATGTTGAGAAGGGTCTACAGTAAAGGGAANCA 655	
Qy	555 ATGCAACAGACTGAGTGTGAGGCAATGCAATTGAGGCTGAAACCTTATTTCA 614	
Db	656 CTGATGTTGATGTTGAAATTTGAGGCAATGCAATTGAGGCTGAAACCTTATTTCA 715	
Qy	615 TACATGGTCACAGAAATGAAAGAATGGTGCGACCTGAAACCTTATTTCA 774	
Db	716 TACTTTTATATACATCAAAAGTGTGAAATGTTGAGGCTGAAACCTTATTTCA 775	
Qy	675 ACGGATAAAAGATGTCACACATCCAGACATTTGCGACTATTTGGGAGTCTAA 734	
Db	776 AGTGAAGAAAGAAATTCTGATTCGTCATGTTGACTCTTGTGAAATGCGAACT 835	
Qy	735 ACCACACGCTGATCTACTATTTGAGATGAGTGTGAGTGTGAGCTTCAACCTT 794	
Db	836 CACCGTAAAGCCTTGTCTATATCTGAAAGTGTGAAATGTTGAGGCTGAAACGACTC 895	
Qy	795 GCTCTGACANGATTCGCGGACTTCATGCGGCTGCAAGGGCAGAGTTGGT 854	
Db	896 GTCTGATGATGCTAAAGTTGTCAGTGTGAGTGTGAGGCTGAAACGAGTTGGT 955	
Qy	855 GATCGTGTAAAGCTGTTGAGACATGTTGAGTGTGAGCTGAGGT 902	
Db	956 TGCACATGAGTAGACGCTTAAAGATGTTGCTACTGTTGCTACTGTTG 1003	
RESULT 1 2		
BG321293	BC321293 977 bp mRNA linear EST 27-FEB-2001	
DEFINITION	Zm04_04909_R Zm04_AAFC_ECORC_cold_stressed_maize_seedlings_Zea_mays	
ACCESSION	Zm04_04909	
VERSION	2	
VERSION	Zm04_04909	
KEYWORDS	mRNA sequence.	
EST.		
SOURCE		
ORGANISM	Zea mays.	
	Bukayoya; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. (bases 1 to 977)	
REFERENCE	Singh,J.A., Wakil,K., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Sprot,D. and Tinker,N.A., 2001. Expressed Sequence Tags from Cold-Stressed Maize Seedlings	
AUTHORS	COMMENT	Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-Food Canada K.W. Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701 Email: singhjaem.agr.ca.

RESULT 13	Db	475	GCCTGTGATGCTGTAAATGTGAACTAAAGCGTAAACCTGTGACCAACCTGAA	534
AL532233	Oy	438	GCTATGCTCAGTCGTCAGTGTGAGTCATCAGCTCTGAAAG---TGGAGCTATC	494
LOCUS	Db	535	GAATTCAGCTGGTCTAGATTCCTGCACCGACAGAAATTGCAATATC	594
DEFINITION	Qy	495	TCAAACGGACAGATGTGATGTTACCCATGAAATCTCCAGT	554
AL532233	Qy	595	TCTGAGCTATGAGCTGGGGCGACAGATGTGATGTTACCCATGAAATCTCCAGT	654
ACCESSION	Db	555	TCTGAGCTATGAGCTGGGGCGACAGATGTGATGTTACCCATGAAATCTCCAGT	654
VERSION	Db	655	CTGAGCTATGAGCTGGGGCGACAGATGTGATGTTACCCATGAAATCTCCAGT	714
KEYWORDS	Db	615	TACATGGTACAGACITGAGGTGAAGGCAATGTACCGTGTACCTGTCAA	614
SOURCE	Db	615	TACATGGTACAGACITGAGGTGAAGGCAATGTACCGTGTACCTGTCAA	714
Homo sapiens	Qy	715	TACTTATATATATCATCAAAAGTCAGATGTGATGCTTCAGATGCTCGT	774
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy	675	AGGATTAAGAAAGCTGAAACATCCAGACTTTGGCFACTACTTGAGGAATCTAA	734
Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.	Db	775	ATGAAAGAAATTCATATCAGTCAGTGTGATGTTGAAATTCATTCATC	834
REFERENCE	Qy	735	ACCCACCGTCATACTCATATATGAGATATGGGGGGAGACCTTCACCC	794
AUTHORS	Db	835	CACCGTCATCTTGTGCAATGCGAGATGTGATGCTTCAGATGCTCGT	894
Li, W.B.; Gruber,C.; Jesse, J. and Polaves,D.	Qy	795	GCTTGAACAGATGTCACCTGAGCTTGTGACTTCATGTTGCTGTCAGACT	854
TITLE	Db	895	GCTTGAACAGATGTCACCTGAGCTTGTGACTTCATGTTGCTGTCAGACT	889
Full-length cDNA libraries and normalization	Qy	855	GATCGTCGAACATGTCAGTGTGACTTCATGTTGCTGTCAGACT	954
Unpublished (2001)	Db	955	GACAATAGAAAGCAGCTTAAGATATGCTT	988
COMMENT				
Contact: Genoscope				
Genoscope - Centre National de Sequençage				
BP 191 91006 EVRY cedex - France				
Email: seer@genoscope.cns.fr, Web : <a href="http://genoscope.cns.fr">www.genoscope.cns.fr</a> .				
FEATURES				
source				
1. (bases 1 to 988)				
/organism="Homo sapiens"				
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/lab_host="DHIB"				
/note="organ: brain; vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : <a href="mailto:flangef@tech.com">flangef@tech.com</a> ; URL : <a href="http://fulllength.invitrogen.com">http://fulllength.invitrogen.com</a> "				
BASE COUNT	306 a	188 c	242 g	251 t
ORIGIN				1 others
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Best Local Similarity		57.1%	Score 253.4; DB 9; Length 988;	
Matches		500;	Score 253.4; DB 9; Length 988;	
Conservative		0;	Score 253.4; DB 9; Length 988;	
Mismatches		371;	Score 253.4; DB 9; Length 988;	
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Mismatches		371;	Score 253.4; DB 9; Length 988;	
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BASE COUNT	288 a	181 c	236 g	247 t
ORIGIN				3 others
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BASE COUNT	288 a	181 c	236 g	247 t
ORIGIN				3 others
Query Match		15.3%	Score 253.4; DB 9; Length 988;	
Best Local Similarity		57.1%	Score 253.4; DB 9; Length 988;	
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BASE COUNT	288 a	181 c	236 g	247 t
ORIGIN				3 others
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/note="vector: pCMVSPORT 6; site:1: NotI: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : <a href="mailto:flangef@tech.com">flangef@tech.com</a> ; URL : <a href="http://fulllength.invitrogen.com">http://fulllength.invitrogen.com</a> "				
BASE COUNT	288 a	181 c	236 g	247 t
ORIGIN				3 others

ORIGIN		VERSION	KEYWORDS	REFERENCE	AUTHORS	JOURNAL	COMMENT
Query	Match	EST	SOURCE	MATERIAL	TITLE	UNPUBLISHED	CONTACT
Qy	18	GEAAAAGAAATCAAAATTTCAGCAGATCGGGTGTGCATGTCGGCGAGSTGTATG	1	1 (Bases 1 to 1017)			
Db	114	GCCTAAAGAGCTAAATTGGTGCAGATGCCGAGCTTATCCTCAAGGTGAGCTT	173	L.I. W.B., Gruber,C., Jesse,J. and Polayes,D.	Full-length cDNA libraries and normalization		
Qy	78	TTACGAGATACCGTCAAAGTAACTCTGGTGTCTAAAGGCCGAATTGTC	137				
Db	174	TTACGAGATACCGTCAAAGTAACTCTGGTGTCTAAAGGCCGAATTGTC	233				
Qy	138	GTTCGGTGTCTCCCTAAATCTATGACGGGTAACCATGCTAAAGAGATGG	197				
Db	234	AGTGGGGAGTCGCCAACAGTAAAGGAAAGCTGTGACTCTGCAAGTCATGACTA	293				
Qy	198	GAAGACATTTGAAACAGGGCAATTGGTGTGAGTGCCTCTAAACCAAT	257				
Db	294	AAAGATAATACAAACATGGCTAAACTTGTGCAACTTGCCATACAAAT	353				
Qy	258	GATATGCGGTGTATGGAGGACTACTGCAACAGCTTGTACGCAAGCCATTCTGAA	317				
Db	354	GAAGAGCGGGTGTACCCCTCTACTGCTGACGCTATAGCAGGAA	413				
Qy	318	GACTAAATATGACAGAGGGCTATCCTATGTCCTCGGCGAGCTGAA	377				
Db	414	GCCTTCGAGAGATAGTACAGATGGCTTATCCTGAAACATGAGAGGTTGATGTTA	473				
Qy	318	GCACACGCCACACCGTGTGAGCTTGTACCCATTGTCAACCTGATGAA	437				
Db	474	GCTGTGATGCTTGTGACTCATCGAGTTCAGCAACGGAGAACAAATGGCA	533				
Qy	438	GCTATGCTCAGTCCTGAGATCTCGAAACGGAGAACAAATGGCTGAA	494				
Db	534	GAATTCAGCTGAGCTCTAGATTCAGCAACGGAGAACAAATGGCAATTCATC	593				
Qy	495	TCAGAGCATTGAGCTGCGGCAACGAGGGTGTACATCGAGAATCTCGGT	554				
Db	594	TCTGTGCAATGAAAGAATGTTGAGAACGGTGTACAGTAAAGGAA	653				
Qy	555	ATGGAAAGCACTGAACTGAGTGGTGTGAGGATGCAATTGACCTGGTACTCTGTC	614				
Db	654	CTGATGATGAGTGTGAAATTTGAGCCATGTCGATGCTATCTGTTA	713				
Qy	615	TACATGGTCAAGACATGAAATGGTGTGAGGATGCAATTGACCTGGTACTCTGTC	674				
Db	714	TACTTATTAATACAAAGTCAGAAATGTCATTCGGATGCTATCTGTTA	773				
Qy	675	ACGGATAAAGATGTCACACATCCAGACATTTGCCACTACTGAGAATTCTAA	734				
Db	774	AGTGAAGAAGAAATTCTGTATGTCAGTGTGACTCTGCTCTGAGKGCATGT	833				
Qy	735	ACCAACCTTCACTCATCTATGAGATGCTGATGTTGAAAGCTTCCACCT	794				
Db	834	CACCGTAAGCTTGTCAATGCGAGATGTTGATGAAAGCTCTAAGACACT	893				
Qy	795	GTCTGAAAGATGCTGACTTCATGAGCTGCTGCTCAAGGCCGAGTTGGT	854				
Db	894	GTCTGAAAGATGCTAAGGTGCTCAGGTGTCAGGTCAGTGGCGAGCTCAGGTTGGT	953				
Qy	855	GA 856					
Db	954	GA 955					
RESULT 15							
AL515579	AL515579	AL515579 LTL-NFL011-NBC1	1017 bp mRNA	linear	EST 13-FEB-2001		
LOCUS	AL515579	AL515579	Homo sapiens	cDNA clone	CSDA002YD05		
DEFINITION	AL515579	AL515579	prime, mRNA sequence.				
ACCESSION	AL515579	AL515579					

QY	495	TCAGAAGCTATGGAACCGTGTGGCGAACGATGGTGTACCATCGAGAACTCGAGGT	554
Db	596	TCTGTGCAATGAAAGTGGACAGAAGGGTGTCACTCGAGAACTCGAGGT	655
QY	555	ATGGAACAGACTGAGTGGCGACATGCGAATGGTGTACCGGTGTCACAA	614
Db	656	CTGATGATGATGATAATTGAGCTGAGGCTGAGAAGTTGATCGAGGCTTATTCCCA	715
QY	615	TACATGGTCACAGACATGAAAATGGTGGAGACCTGAGAACCATTTCTTATC	674
Db	716	TACTTTAACTTACATCAGAGTCAGAAATGTAATTGAGTCAGATCCATGTCGTTG	775
QY	675	ACGGATAAAAGTCACACTCCAGACATTTCCACTACTGGAGAGTCCTAA	734
Db	776	AGTAAAGAGAATTCAGTATCCAGTCAGTGTACCTGCTTAAATGCAATGCT	835
QY	735	ACCCACCGTCCATACATCATGAGATGATGAGGGGAGACCTTCACCTT	794
Db	836	CACCGTAAAGCTTGGCATATCCTGAGATGTTGAGAAGCTTAAGTACTC	895
QY	795	GTCITGACAGAATTCGGFACTTCATGTTGTCGTCAGCGCAGATTGGT	854
Db	896	GTCITGAACTGGCTAAGGTTGGCTCAGGTGGCGTAAGCCCTCAGGTGGT	955
QY	855	GA 856	
Db	956	GA 957	

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 Job time : 2499.54 secs